

Supplementary Information

Rationally Designing Aptamer Sequences with Reduced Affinity for Controlled Sensor Performance. *Sensors* 2015, 15, 7754-7767

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Table S1. All of the lowest energy secondary structures for the novel aminoglycoside aptamer sequence. All of the structures were determined by using MFOLD and were done based on the aptamer in a 1 M NaCl solution at 25 °C [1,2].

Sequence Name	Secondary Structure Prediction	Folding Energy (kcal/mol)
7UG		-0.64
7UC		-0.64

Table S1. Cont.

Sequence Name	Secondary Structure Prediction	Folding Energy (kcal/mol)
16GU		-2.13
3-UAC		-1.60

References

1. Zuker, M. Mfold web server for nucleic acid folding and hybridization prediction. *Nucleic Acids Res.* **2003**, *31*, 3406–3415.
2. Zuker, M.; Jacobson, A.B. Using reliability information to annotate RNA secondary structures. *Using reliability information to annotate RNA secondary structures. RNA* **1998**, *4*, 669–679.

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